



SN 09-267963.ST25.txt  
SEQUENCE LISTING

<110> MIYAZONO, Kohei  
IMAMURA, Takeshi  
DEN DIJKE, Peter

<120> PROTEINS HAVING SERINE/THREONINE KINASE DOMAINS, CORRESPONDING NUCLEIC ACID MOLECULES AND THEIR USE

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<141> 1999-03-12

<150> PCT/GB93/02367  
<151> 1993-11-17

<150> US 09/039,177  
<151> 1998-03-13

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Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr  
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Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr  
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Val Tyr Ile Cys His Asn Arg Thr Val Ile His His Arg Val Pro Asn  
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cgcacatgtgcc	gaggtgtgtc	ccacattgtg	cctggctgt	gccacgccc	tgtgtgtgt	2100
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&lt;210&gt; 16

&lt;211&gt; 505

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 16

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1				5					10				15		

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								25					30		

Leu	Cys	Ala	Cys	Thr	Ser	Cys	Leu	Gln	Thr	Asn	Tyr	Thr	Cys	Glu	Thr
	35						40				45				

Asp	Gly	Ala	Cys	Met	Val	Ser	Ile	Phe	Asn	Leu	Asp	Gly	Val	Glu	His
				50		55					60				

His	Val	Arg	Thr	Cys	Ile	Pro	Lys	Val	Glu	Leu	Val	Pro	Ala	Gly	Lys
				65			70		75				80		

Pro	Phe	Tyr	Cys	Leu	Ser	Ser	Glu	Asp	Leu	Arg	Asn	Thr	His	Cys	Cys
				85				90				95			

Tyr	Ile	Asp	Phe	Cys	Asn	Lys	Ile	Asp	Leu	Arg	Val	Pro	Ser	Gly	His
				100			105				110				

Leu	Lys	Glu	Pro	Ala	His	Pro	Ser	Met	Trp	Gly	Pro	Val	Glu	Leu	Val
					115			120				125			

Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile  
 130 135 140

Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln  
 145 150 155 160

Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp  
 165 170 175

Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly  
 180 185 190

Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val  
 195 200 205

Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly  
 210 215 220

Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu  
 225 230 235 240

Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu  
 245 250 255

Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn  
 260 265 270

Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly  
 275 280 285

Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met  
 290 295 300

Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met  
 305 310 315 320

Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu  
 325 330 335

Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala  
 340 345 350

Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp  
 355 360 365

Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu  
 370 375 380

Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys  
 385 390 395 400

Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg  
 405 410 415

Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp  
 420 425 430

Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys  
 435 440 445

Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln Ser Tyr Glu  
 450 455 460

Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn  
 465 470 475 480

Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln  
 485 490 495

Leu Ser Val Gln Glu Asp Val Lys Ile  
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gaagatgact	ctggaatgcc	tgttgtcacc	tctggatgtc	taggactaga	agggtcagat	420
tttcaatgtc	gtgacactcc	cattcctcat	caaagaagat	caattgaatg	ctgcacagaa	480
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 tggatggaa agtggcgtgg agaaaaggtg gctgtgaaag tttcttcac cacggagaa 900  
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 cacggtggc agacacagag gaacccagaa acacggattc atcatggctt tctgaggagg 1860  
 agaaactgtt tggtaactt gttcaagata tcatgcgtt tgctttctaa gaaagccctg 1920  
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 <211> 502  
 <212> PRT  
 <213> Mus musculus

<400> 18

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 20 25 30

Lys Cys His His Cys Pro Glu Asp Ser Val Asn Asn Ile Cys Ser  
 35 40 45

## SN 09-267963.ST25.txt

Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser Gly Met  
 50 55 60

Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp Phe Gln  
 65 70 75 80

Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys  
 85 90 95

Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro  
 100 105 110

Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys Ala Leu  
 115 120 125

Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile Ile Leu  
 130 135 140

Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg Tyr Ser  
 145 150 155 160

Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu Ser Leu  
 165 170 175

Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu  
 180 185 190

Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys  
 195 200 205

Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg  
 210 215 220

Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser  
 225 230 235 240

Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu  
 245 250 255

Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp  
 260 265 270

Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr  
 275 280 285

Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu Lys Leu  
 290 295 300

Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu Ile Phe  
305 310 315 320

Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys  
325 330 335

Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu Gly  
340 345 350

Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro  
355 360 365

Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val Leu Asp  
370 375 380

Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala Asp Met  
385 390 395 400

Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys Val Ser  
405 410 415

Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro  
420 425 430

Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met Lys Lys  
435 440 445

Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys Leu Arg  
450 455 460

Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro Ala Ser  
465 470 475 480

Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met Ser Glu  
485 490 495

Ser Gln Asp Ile Lys Leu  
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<210> 19  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Sense primer, extracellular domain.

<220>

78

F

SN 09-267963.ST25.txt

<221> misc\_feature  
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<223> The nucleotide at position 20 may be any nucleotide

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gcggatccctg ttgtgaaggn aatatgtg

28

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<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Sense primer, kinase domain II

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gcgatccgtc gcagtcaaaa tttt

24

<210> 21  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Sense Primer, Kinase domain VIB

<400> 21  
gcggatccgc gatatattaa aagcaa

26

<210> 22  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Anti-sense primer, Kinase Domain VIB

<400> 22  
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20

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<210> 23  
<211> 37  
<212> DNA  
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<220>  
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<400> 23  
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37

<210> 24  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5' oligonucleotide primer

<400> 24  
gcggatccac catggcggag tcggcc

26

<210> 25  
<211> 20  
<212> DNA  
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<220>  
<223> 3' oligonucleotide primer

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aacaccgggc cggcgatgtat

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<210> 26  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus sequence in Subdomain I

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<223> Xaa at position 2 may be any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (4)..(5)  
<223> Xaa at position 4 and 5 may be any amino acid

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Gly Xaa Gly Xaa Xaa Gly  
1 5

<210> 27  
<211> 6  
<212> PRT  
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<400> 27

Asp Phe Lys Ser Arg Asn  
1 5

<210> 28  
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<212> PRT  
<213> Homo sapiens

<400> 28

Asp Leu Lys Ser Lys Asn  
1 5

<210> 29  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 29

Gly Thr Lys Arg Tyr Met  
1 5

<210> 30  
<211> 182  
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<213> Homo sapiens

<400> 30

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Lys Leu Lys Gln Asn Thr Ser Glu Gln Phe Glu Thr Val Ala Val Lys  
20 25 30

Ile Phe Pro Tyr Asp His Tyr Ala Ser Trp Lys Asp Arg Lys Asp Ile  
35 40 45

Phe Ser Asp Ile Asn Leu Lys His Glu Asn Ile Leu Gln Phe Leu Thr  
50 55 60

Ala Glu Glu Arg Lys Thr Glu Leu Gly Lys Gln Tyr Trp Leu Ile Thr  
65 70 75 80

Ala Phe His Ala Lys Gly Asn Leu Gln Glu Tyr Leu Thr Arg His Val  
85 90 95

Ile Ser Trp Glu Asp Leu Arg Asn Val Gly Ser Ser Leu Ala Arg Gly  
100 105 110

Leu Ser His Leu His Ser Asp His Thr Pro Cys Gly Arg Pro Lys Met  
115 120 125

Pro Ile Val His Arg Asp Leu Lys Ser Ser Asn Ile Leu Val Lys Asn  
130 135 140

Asp Leu Thr Cys Cys Leu Cys Asp Phe Gly Leu Ser Leu Arg Leu Gly  
145 150 155 160

Pro Tyr Ser Ser Val Asp Asp Leu Ala Asn Ser Gly Gln Val Gly Thr  
165 170 175

Ala Arg Tyr Met Ala Pro  
180

<210> 31  
<211> 176  
<212> PRT  
<213> Mus musculus

<400> 31

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20 25 30

Lys Gln Ser Trp Gln Ser Glu Arg Glu Ile Phe Ser Thr Pro Gly Met  
35 40 45

Lys His Glu Asn Leu Leu Gln Phe Ile Ala Ala Glu Lys Arg Gly Ser  
50 55 60

Asn Leu Glu Val Glu Leu Trp Leu Ile Thr Ala Phe His Asp Lys Gly  
65 70 75 80

Ser Leu Thr Asp Tyr Leu Lys Gly Asn Ile Ile Thr Trp Asn Glu Leu  
85 90 95

Cys His Val Ala Glu Thr Met Ser Arg Gly Leu Ser Tyr Leu His Glu  
100 105 110

Asp Val Pro Trp Cys Arg Gly Glu Gly His Lys Pro Ser Ile Ala His  
115 120 125

Arg Asp Phe Lys Ser Lys Asn Val Leu Leu Lys Ser Asp Leu Thr Ala  
130 135 140

Val Leu Ala Asp Phe Gly Leu Ala Val Arg Phe Glu Pro Gly Lys Pro  
145 150 155 160

Pro Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro  
165 170 175

<210> 32  
<211> 175  
<212> PRT  
<213> Mus musculus

<400> 32

Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala  
Page 36

g2

g2

Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln Asp  
20 25 30

Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly Met  
35 40 45

Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly Thr  
50 55 60

Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys Gly  
65 70 75 80

Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu Leu  
85 90 95

Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His Glu  
100 105 110

Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His Arg  
115 120 125

Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala Cys  
130 135 140

Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser Ala  
145 150 155 160

Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro  
165 170 175

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Asp Tyr Arg Gly Glu Ala Val Ala Val Lys Val Phe Asn Ala Leu Asp  
20 25 30

Glu Pro Ala Phe His Lys Glu Thr Glu Ile Phe Glu Thr Arg Met Leu  
35 40 45

Arg His Pro Asn Val Leu Arg Tyr Ile Gly Ser Asp Arg Val Asp Thr  
Page 37

23

CD

50

55

60

Gly Phe Val Thr Glu Leu Trp Leu Val Thr Glu Tyr His Pro Ser Gly  
 65 70 75 80

Ser Leu His Asp Phe Leu Leu Glu Asn Thr Val Asn Ile Glu Thr Tyr  
 85 90 95

Tyr Asn Leu Met Arg Ser Thr Ala Ser Gly Leu Ala Phe Leu His Asn  
 100 105 110

Gln Ile Gly Gly Ser Lys Glu Ser Asn Lys Pro Ala Met Ala His Arg  
 115 120 125

Asp Ile Lys Ser Lys Asn Ile Met Val Lys Asn Asp Leu Thr Cys Ala  
 130 135 140

Ile Gly Asp Leu Gly Leu Ser Leu Ser Lys Pro Glu Asp Ala Ala Ser  
 145 150 155 160

Asp Ile Ile Ala Asn Glu Asn Tyr Lys Cys Gly Thr Val Arg Tyr Leu  
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Ala Pro

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Cont

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<211> 513

<212> PRT

<213> Mus musculus

<400> 34

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 20 25 30

Phe Asn Ala Asn Trp Glu Lys Asp Arg Thr Asn Gln Thr Gly Val Glu  
 35 40 45

Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp  
 50 55 60

Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu  
 65 70 75 80

Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu Lys Lys Asp  
 Page 38

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Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu  
100 105 110

Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn  
115 120 125

Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu  
130 135 140

Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala Phe Trp Val  
145 150 155 160

Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln  
165 170 175

Asp Pro Gly Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu  
180 185 190

Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys  
195 200 205

Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln  
210 215 220

Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly  
225 230 235 240

Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly  
245 250 255

Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys  
260 265 270

Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu  
275 280 285

Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His  
290 295 300

Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His  
305 310 315 320

Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala  
325 330 335

VS

1

Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser  
 340 345 350

Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro  
 355 360 365

Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg  
 370 375 380

Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg  
 385 390 395 400

Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu  
 405 410 415

Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val  
 420 425 430

Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His  
 435 440 445

Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His  
 450 455 460

Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr  
 465 470 475 480

*j2*  
 Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr  
 485 490 495

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 Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser  
 500 505 510

Leu

<210> 35  
 <211> 536  
 <212> PRT  
 <213> Mus musculus

<400> 35

Met Thr Ala Pro Trp Ala Ala Leu Ala Leu Leu Trp Gly Ser Leu Cys  
 1 5 10 15

Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr  
 20 25 30

Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg  
 35 40 45

Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Arg  
 50 55 60

Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp  
 65 70 75 80

Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn  
 85 90 95

Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg  
 100 105 110

Phe Thr His Leu Pro Glu Pro Gly Gly Pro Glu Val Thr Tyr Glu Pro  
 115 120 125

Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu  
 130 135 140

Pro Ile Gly Gly Leu Ser Leu Ile Val Leu Leu Ala Phe Trp Met Tyr  
 145 150 155 160

Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Val Arg  
 165 170 175

*32*  
*cont*  
 Gln Cys Gln Arg Trp Ala Gly Arg Asp Gly Cys Ala Asp Ser Phe  
 180 185 190

Lys Pro Leu Pro Phe Gln Asp Pro Gly Pro Pro Pro Ser Pro Leu  
 195 200 205

Val Gly Leu Lys Pro Leu Gln Leu Leu Glu Ile Lys Ala Arg Gly Arg  
 210 215 220

Phe Gly Cys Val Trp Lys Ala Gln Leu Met Asn Asp Phe Val Ala Val  
 225 230 235 240

Lys Ile Phe Pro Leu Gln Asp Lys Gln Ser Trp Gln Ser Glu Arg Glu  
 245 250 255

Ile Phe Ser Thr Pro Gly Met Lys His Glu Asn Leu Leu Gln Phe Ile  
 260 265 270

Ala Ala Glu Lys Arg Gly Ser Asn Leu Glu Val Glu Leu Trp Leu Ile  
 275 280 285

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Thr Ala Phe His Asp Lys Gly Ser Leu Thr Asp Tyr Leu Lys Gly Asn  
290 295 300

Ile Ile Thr Trp Asn Glu Leu Cys His Val Ala Glu Thr Met Ser Arg  
305 310 315 320

Gly Leu Ser Tyr Leu His Glu Asp Val Pro Trp Cys Arg Gly Glu Gly  
325 330 335

His Lys Pro Ser Ile Ala His Arg Asp Phe Lys Ser Lys Asn Val Leu  
340 345 350

Leu Lys Ser Asp Leu Thr Ala Val Leu Ala Asp Phe Gly Leu Ala Val  
355 360 365

Arg Phe Glu Pro Gly Lys Pro Pro Gly Asp Thr His Gly Gln Val Gly  
370 375 380

Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe  
385 390 395 400

Gln Arg Asp Ala Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val  
405 410 415

Leu Trp Glu Leu Val Ser Arg Cys Lys Ala Ala Asp Gly Pro Val Asp  
420 425 430

Glu Tyr Met Leu Pro Phe Glu Glu Ile Gly Gln His Pro Ser Leu  
435 440 445

Glu Glu Leu Gln Glu Val Val His Lys Lys Met Arg Pro Thr Ile  
450 455 460

Lys Asp His Trp Leu Lys His Pro Gly Leu Ala Gln Leu Cys Val Thr  
465 470 475 480

Ile Glu Glu Cys Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly  
485 490 495

Cys Val Glu Glu Arg Val Ser Leu Ile Arg Arg Ser Val Asn Gly Thr  
500 505 510

Thr Ser Asp Cys Leu Val Ser Leu Val Thr Ser Val Thr Asn Val Asp  
515 520 525

Leu Leu Pro Lys Glu Ser Ser Ile  
530 535

<210> 36  
 <211> 567  
 <212> PRT  
 <213> Homo sapiens

<400> 36

Met Gly Arg Gly Leu Leu Arg Gly Leu Trp Pro Leu His Ile Val Leu  
 1 5 10 15

Trp Thr Arg Ile Ala Ser Thr Ile Pro Pro His Val Gln Lys Ser Val  
 20 25 30

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro  
 35 40 45

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln  
 50 55 60

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro  
 65 70 75 80

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr  
 85 90 95

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile  
 100 105 110

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys  
 115 120 125

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn  
 130 135 140

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu  
 145 150 155 160

Leu Leu Val Ile Phe Gln Val Thr Gly Ile Ser Leu Leu Pro Pro Leu  
 165 170 175

Gly Val Ala Ile Ser Val Ile Ile Ile Phe Tyr Cys Tyr Arg Val Asn  
 180 185 190

Arg Gln Gln Lys Leu Ser Ser Thr Trp Glu Thr Gly Lys Thr Arg Lys  
 195 200 205

Leu Met Glu Phe Ser Glu His Cys Ala Ile Ile Leu Glu Asp Asp Arg  
 210 215 220

24

Ser Asp Ile Ser Ser Thr Cys Ala Asn Asn Ile Asn His Asn Thr Glu  
225 230 235 240

Leu Leu Pro Ile Glu Leu Asp Thr Leu Val Gly Lys Gly Arg Phe Ala  
245 250 255

Glu Val Tyr Lys Ala Lys Leu Lys Gln Asn Thr Ser Glu Gln Phe Glu  
260 265 270

Thr Val Ala Val Lys Ile Phe Pro Tyr Glu Glu Tyr Ala Ser Trp Lys  
275 280 285

Thr Glu Lys Asp Ile Phe Ser Asp Ile Asn Leu Lys His Glu Asn Ile  
290 295 300

Leu Gln Phe Leu Thr Ala Glu Glu Arg Lys Thr Glu Leu Gly Lys Gln  
305 310 315 320

Tyr Trp Leu Ile Thr Ala Phe His Ala Lys Gly Asn Leu Gln Glu Tyr  
325 330 335

Leu Thr Arg His Val Ile Ser Trp Glu Asp Leu Arg Lys Leu Gly Ser  
340 345 350

*g2*  
Cont  
Ser Leu Ala Arg Gly Ile Ala His Leu His Ser Asp His Thr Pro Cys  
355 360 365

Gly Arg Pro Lys Met Pro Ile Val His Arg Asp Leu Lys Ser Ser Asn  
370 375 380

Ile Leu Val Lys Asn Asp Leu Thr Cys Cys Leu Cys Asp Phe Gly Leu  
385 390 395 400

Ser Leu Arg Leu Asp Pro Thr Leu Ser Val Asp Asp Leu Ala Asn Ser  
405 410 415

Gly Gln Val Gly Thr Ala Arg Tyr Met Ala Pro Glu Val Leu Glu Ser  
420 425 430

Arg Met Asn Leu Glu Asn Ala Glu Ser Phe Lys Gln Thr Asp Val Tyr  
435 440 445

Ser Met Ala Leu Val Leu Trp Glu Met Thr Ser Arg Cys Asn Ala Val  
450 455 460

Gly Glu Val Lys Asp Tyr Glu Pro Pro Phe Gly Ser Lys Val Arg Glu  
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465

470

475

480

His Pro Cys Val Glu Ser Met Lys Asp Asn Val Leu Arg Asp Arg Gly  
 485 490 495

Arg Pro Glu Ile Pro Ser Phe Trp Leu Asn His Gln Gly Ile Gln Met  
 500 505 510

Val Cys Glu Thr Leu Thr Glu Cys Trp Asp His Asp Pro Glu Ala Arg  
 515 520 525

Leu Thr Ala Gln Cys Val Ala Glu Arg Phe Ser Glu Leu Glu His Leu  
 530 535 540

Asp Arg Leu Ser Gly Arg Ser Cys Ser Glu Glu Lys Ile Pro Glu Asp  
 545 550 555 560

Gly Ser Leu Asn Thr Thr Lys  
 565

<210> 37

<211> 97

<212> PRT

<213> *Caenorhabditis elegans*

<400> 37

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Cys His Cys Ser Arg Glu Val Gly Cys Asn Ala Arg Thr Thr Gly Trp  
 1 5 10 15

Val Pro Gly Ile Glu Phe Leu Asn Glu Thr Asp Arg Ser Phe Tyr Glu  
 20 25 30

Asn Thr Cys Tyr Thr Asp Gly Ser Cys Tyr Gln Ser Ala Arg Pro Ser  
 35 40 45

Pro Glu Ile Ser His Phe Gly Cys Met Asp Glu Lys Ser Val Thr Asp  
 50 55 60

Glu Thr Glu Phe His Asp Thr Ala Ala Lys Val Cys Thr Asn Asn Thr  
 65 70 75 80

Lys Asp Pro His Ala Thr Val Trp Ile Cys Cys Asp Lys Gly Asn Phe  
 85 90 95

Cys

<210> 38

91

91

<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Serine/threonine kinase consensus

<400> 38

Asp Leu Lys Pro Glu Asn  
1 5

<210> 39  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Tyrosine kinase consensus

<400> 39

Asp Leu Ala Ala Arg Asn  
1 5

<210> 40  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Act R-II motif

<400> 40

Asp Ile Lys Ser Lys Asn  
1 5

<210> 41  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Act R-IIB motif

<400> 41

Asp Phe Lys Ser Lys Asn  
1 5

<210> 42  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> T $\beta$ R-II motif

&lt;400&gt; 42

Asp Leu Lys Ser Ser Asn  
1 5

&lt;210&gt; 43

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Artificial Peptide

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (2)..(2)

&lt;223&gt; Xaa at position 2 is Thr or Ser

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (3)..(4)

&lt;223&gt; Xaa at position three and four can be any amino acid

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (5)..(5)

&lt;223&gt; Xaa at position five is Tyr or Phe

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (6)..(6)

&lt;223&gt; Xaa at position six may be any amino acid

&lt;400&gt; 43

Gly Xaa Xaa Xaa Xaa Xaa  
1 5

&lt;210&gt; 44

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic peptide

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (1)..(1)

&lt;223&gt; Xaa at position 1 is any amino acid

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (3)..(3)

&lt;223&gt; Xaa at position 3 is Ile or Val

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (4)..(4)

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<223> Xaa at position 4 is Lys or Arg

<220>

<221> MISC\_FEATURE

<222> (6)..(6)

<223> Xaa at position 6 is Thr or Met.

<400> 44

Xaa Pro Xaa Xaa Trp Xaa  
1 5

<210> 45

<211> 6

<212> PRT

<213> Homo sapiens

<400> 45

Gly Thr Arg Arg Tyr Met  
1 5

*f2*  
<210> 46

<211> 6

<212> PRT

<213> Homo sapiens

<400> 46

Gly Thr Ala Arg Tyr Met  
1 5